

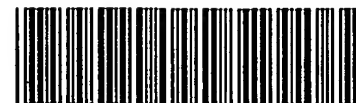
#6

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/520,783
Source: PG/10
Date Processed by STIC: 1/19/05

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 01/19/2005

PATENT APPLICATION: US/10/520,783

TIME: 12:00:55

Input Set : A:\3083us0p.seq.txt

Output Set: N:\CRF4\01192005\J520783.raw

3 <110> APPLICANT: MATSUZAWA, Yuji
 4 FUNAHASHI, Toru
 5 SHIMOMURA, Ichirou
 6 FURUYAMA, Naoki
 8 <120> TITLE OF INVENTION: Novel Proteins and Use Thereof
 10 <130> FILE REFERENCE: 3083USOP
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/520,783
 C--> 12 <141> CURRENT FILING DATE: 2005-01-10
 12 <150> PRIOR APPLICATION NUMBER: PCT/JP03/08690
 13 <151> PRIOR FILING DATE: 2003-07-09
 15 <150> PRIOR APPLICATION NUMBER: JP 2002-201856
 16 <151> PRIOR FILING DATE: 2002-07-10
 18 <160> NUMBER OF SEQ ID NOS: 48
 20 <170> SOFTWARE: PatentIn version 3.1
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 1836
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Mus musculus
 27 <220> FEATURE:
 28 <221> NAME/KEY: CDS
 29 <222> LOCATION: (1)..(1833)
 30 <223> OTHER INFORMATION:
 32 <220> FEATURE:
 33 <221> NAME/KEY: sig_peptide
 34 <222> LOCATION: (1)..(69)
 35 <223> OTHER INFORMATION:
 W--> 37 <220>
 38 <221> NAME/KEY: mat_peptide
 39 <222> LOCATION: (70)..()
 40 <223> OTHER INFORMATION:
 W--> 42 <220>
 43 <221> NAME/KEY: misc_feature
 44 <222> LOCATION: (798)..(798)
 45 <223> OTHER INFORMATION: 'n' stands for unidentified base.
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 51 -20 -15 -10
 53 ttc ctg ggc cct gtg ctg cct gtg agg gca cct gtg ttt ggc cga agt 96
 54 Phe Leu Gly Pro Val Leu Pro Val Arg Ala Pro Val Phe Gly Arg Ser
 55 -5 -1 1 5
 57 gac acc ccc acc ctg agc ccc gag gag aat gaa ttt gtg gag gaa gag 144
 58 Asp Thr Pro Thr Leu Ser Pro Glu Glu Asn Glu Phe Val Glu Glu Glu

P.6

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Input Set : A:\3083us0p.seq.txt

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61 aat cag cca gtg ctg gtt ctg agc tcc gag gag cca gag cct ggc cca      192
62 Asn Gln Pro Val Leu Val Leu Ser Ser Glu Glu Pro Glu Pro Gly Pro
63          30          35          40
65 gcc act gtc gac tgt ccc cga gat tgt gcc tgt tcc cag gaa ggt gta      240
66 Ala Thr Val Asp Cys Pro Arg Asp Cys Ala Cys Ser Gln Glu Gly Val
67          45          50          55
69 gtg gac tgt ggt ggc att gac ctg cgt gag ttt cca ggc gac ctg ccc      288
70 Val Asp Cys Gly Gly Ile Asp Leu Arg Glu Phe Pro Gly Asp Leu Pro
71          60          65          70
73 gag cac acc aac cat ctc tcc ttg cag aac aac cag ctg gag aag atc      336
74 Glu His Thr Asn His Leu Ser Leu Gln Asn Asn Gln Leu Glu Lys Ile
75          75          80          85
77 tac ccc gag gag ctg tcc cgg ctg cag cgg ctg gag acg ctg aac ctg      384
78 Tyr Pro Glu Glu Leu Ser Arg Leu Gln Arg Leu Glu Thr Leu Asn Leu
79 90          95          100          105
81 cag aac aac cgc ctg aca tcc cga ggg ctc cca gag gag gca ttt gag      432
82 Gln Asn Asn Arg Leu Thr Ser Arg Gly Leu Pro Glu Glu Ala Phe Glu
83          110          115          120
85 cat ctt act agc ctc aat tac ctg tac ctg gcc aac aac aag ctg aca      480
86 His Leu Thr Ser Leu Asn Tyr Leu Tyr Leu Ala Asn Asn Lys Leu Thr
87          125          130          135
89 ctg gca ccc cga ttc ctg cca aac gcc ctg atc agt gtg gac ttt gct      528
90 Leu Ala Pro Arg Phe Leu Pro Asn Ala Leu Ile Ser Val Asp Phe Ala
91          140          145          150
93 gcc aat tat ctc act aag atc tat gga ctc acc ttt ggc caa aag cca      576
94 Ala Asn Tyr Leu Thr Lys Ile Tyr Gly Leu Thr Phe Gly Gln Lys Pro
95          155          160          165
97 aat ctg agg tct gtg tac ctg cat aac aac aag cta gca gat gcc ggg      624
98 Asn Leu Arg Ser Val Tyr Leu His Asn Asn Lys Leu Ala Asp Ala Gly
99 170          175          180          185
101 ctg ccg gac cac atg ttc aat ggc tcc agc aac gtc gag atc cta atc      672
102 Leu Pro Asp His Met Phe Asn Gly Ser Ser Asn Val Glu Ile Leu Ile
103          190          195          200
105 ctg tcc agc aac ttc ctg cgc cat gtg ccc aag cac ctg cca ccc gct      720
106 Leu Ser Ser Asn Phe Leu Arg His Val Pro Lys His Leu Pro Pro Ala
107          205          210          215
109 ctg tac aag ctg cac ctc aag aac aat aag cta gag aag atc ccc cct      768
110 Leu Tyr Lys Leu His Leu Lys Asn Asn Lys Leu Glu Lys Ile Pro Pro
111          220          225          230
W--> 113 ggg gcc ttc agt gag ctg agc aac cta cgn gaa ctc tac ctg cag aac      816
114 Gly Ala Phe Ser Glu Leu Ser Asn Leu Arg Glu Leu Tyr Leu Gln Asn
115          235          240          245
117 aac tac ctg acc gac gag ggt ctg gac aac gag acc ttc tgg aag ctg      864
118 Asn Tyr Leu Thr Asp Glu Gly Leu Asp Asn Glu Thr Phe Trp Lys Leu
119 250          255          260          265
121 tcc agc ctg gag tac ctg gac ttg tcc agc acc aac ctg tcg agg gtc      912
122 Ser Ser Leu Glu Tyr Leu Asp Leu Ser Ser Thr Asn Leu Ser Arg Val
123          270          275          280

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125	cca	gcg	ggt	ctt	ccc	cgc	agc	ctg	gtc	ctg	ctg	cac	ctg	gag	aaa	aat	960
126	Pro	Ala	Gly	Leu	Pro	Arg	Ser	Leu	Val	Leu	Leu	His	Leu	Glu	Lys	Asn	
127				285					290					295			
129	gcc	atc	cag	agc	gta	gaa	gct	gat	gtg	ctg	aca	ccc	atc	cgc	aac	ctg	1008
130	Ala	Ile	Gln	Ser	Val	Glu	Ala	Asp	Val	Leu	Thr	Pro	Ile	Arg	Asn	Leu	
131			300					305					310				
133	gag	tac	ctg	ctg	cta	cat	agc	aac	cag	ctg	cag	gcc	aag	ggt	atc	cac	1056
134	Glu	Tyr	Leu	Leu	Leu	His	Ser	Asn	Gln	Leu	Gln	Ala	Lys	Gly	Ile	His	
135		315					320					325					
137	cca	ctg	gcc	ttc	cag	ggc	ctc	aag	aag	ctc	cac	aca	gtg	cat	cta	tac	1104
138	Pro	Leu	Ala	Phe	Gln	Gly	Leu	Lys	Lys	Leu	His	Thr	Val	His	Leu	Tyr	
139	330					335						340				345	
141	aac	aac	gcg	ctg	gaa	cgt	gtg	ccc	agc	ggc	ctg	ccc	cgc	cga	gtg	cgc	1152
142	Asn	Asn	Ala	Leu	Glu	Arg	Val	Pro	Ser	Gly	Leu	Pro	Arg	Arg	Val	Arg	
143					350					355					360		
145	acc	ctc	atg	atc	ctg	cac	aac	cag	att	aca	ggc	ata	ggc	cgt	gag	gac	1200
146	Thr	Leu	Met	Ile	Leu	His	Asn	Gln	Ile	Thr	Gly	Ile	Gly	Arg	Glu	Asp	
147			365						370				375				
149	ttc	gct	acc	acc	tac	ttc	ctg	gaa	gag	ctc	aac	ctc	agc	tac	aac	cgc	1248
150	Phe	Ala	Thr	Thr	Tyr	Phe	Leu	Glu	Glu	Leu	Asn	Leu	Ser	Tyr	Asn	Arg	
151			380					385					390				
153	atc	acc	agc	cca	cag	atg	cac	cga	gat	gcc	ttc	cgc	aag	cta	cgc	ctg	1296
154	Ile	Thr	Ser	Pro	Gln	Met	His	Arg	Asp	Ala	Phe	Arg	Lys	Leu	Arg	Leu	
155		395					400					405					
157	ctg	cgt	tca	ctt	gac	ttg	tct	ggc	aac	cgt	ctg	caa	aca	ctg	cct	cca	1344
158	Leu	Arg	Ser	Leu	Asp	Leu	Ser	Gly	Asn	Arg	Leu	Gln	Thr	Leu	Pro	Pro	
159	410					415					420					425	
161	ggc	ctg	ccg	aaa	aac	gta	cac	gtg	ctc	aag	gtc	aag	cgg	aat	gag	ctg	1392
162	Gly	Leu	Pro	Lys	Asn	Val	His	Val	Leu	Lys	Val	Lys	Arg	Asn	Glu	Leu	
163				430						435					440		
165	gct	gcc	ctg	gca	cgt	ggg	gca	cta	gct	ggc	atg	gcc	cag	ctt	cgg	gaa	1440
166	Ala	Ala	Leu	Ala	Arg	Gly	Ala	Leu	Ala	Gly	Met	Ala	Gln	Leu	Arg	Glu	
167				445					450					455			
169	ctc	tac	ctc	aca	ggc	aac	cga	ctg	cga	agc	cgg	gcc	ctg	gga	ccc	cgt	1488
170	Leu	Tyr	Leu	Thr	Gly	Asn	Arg	Leu	Arg	Ser	Arg	Ala	Leu	Gly	Pro	Arg	
171			460					465					470				
173	gcc	tgg	gtg	gac	ctt	gct	ggt	ctg	cag	ctg	ctg	gac	atc	gct	ggg	aat	1536
174	Ala	Trp	Val	Asp	Leu	Ala	Gly	Leu	Gln	Leu	Leu	Asp	Ile	Ala	Gly	Asn	
175		475					480					485					
177	cag	ctc	aca	gag	gtc	cct	gag	ggg	ctc	ccc	cca	tct	ctg	gag	tat	ctg	1584
178	Gln	Leu	Thr	Glu	Val	Pro	Glu	Gly	Leu	Pro	Pro	Ser	Leu	Glu	Tyr	Leu	
179	490					495					500					505	
181	tac	ctg	cag	aat	aac	aag	att	agt	gcc	gtt	cct	gcc	aac	gcc	ttt	gac	1632
182	Tyr	Leu	Gln	Asn	Asn	Lys	Ile	Ser	Ala	Val	Pro	Ala	Asn	Ala	Phe	Asp	
183				510						515					520		
185	tcc	act	ccc	aac	ctt	aag	ggg	atc	ttt	ctc	agg	ttc	aac	aag	ctg	gct	1680
186	Ser	Thr	Pro	Asn	Leu	Lys	Gly	Ile	Phe	Leu	Arg	Phe	Asn	Lys	Leu	Ala	
187				525						530				535			
189	gtg	ggc	tcc	gtg	gtg	gaa	agc	gcc	ttc	cgg	agg	ctg	aaa	cac	ctg	cag	1728

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Input Set : A:\3083us0p.seq.txt

Output Set: N:\CRF4\01192005\J520783.raw

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190 Val Gly Ser Val Val Glu Ser Ala Phe Arg Arg Leu Lys His Leu Gln
191          540          545          550
193 gtc ttg gac att gaa ggc aac ttt gag ttt ggt aat ggt tcc aag gac      1776
194 Val Leu Asp Ile Glu Gly Asn Phe Glu Phe Gly Asn Gly Ser Lys Asp
195          555          560          565
197 aaa gat gag gaa gag gaa gaa gag gag gaa gag gaa gat gag gaa gag      1824
198 Lys Asp Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Asp Glu Glu Glu
199 570          575          580          585
201 gaa act aga tag      1836
202 Glu Thr Arg
206 <210> SEQ ID NO: 2
207 <211> LENGTH: 611
208 <212> TYPE: PRT
209 <213> ORGANISM: Mus musculus
211 <400> SEQUENCE: 2
213 Met Ala Gly Ser Arg Gly Leu Pro Leu Leu Leu Leu Val Leu Gln Leu
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217 Phe Leu Gly Pro Val Leu Pro Val Arg Ala Pro Val Phe Gly Arg Ser
218          -5          -1 1          5
221 Asp Thr Pro Thr Leu Ser Pro Glu Glu Asn Glu Phe Val Glu Glu Glu
222 10          15          20          25
225 Asn Gln Pro Val Leu Val Leu Ser Ser Glu Glu Pro Glu Pro Gly Pro
226          30          35          40
229 Ala Thr Val Asp Cys Pro Arg Asp Cys Ala Cys Ser Gln Glu Gly Val
230          45          50          55
233 Val Asp Cys Gly Gly Ile Asp Leu Arg Glu Phe Pro Gly Asp Leu Pro
234          60          65          70
237 Glu His Thr Asn His Leu Ser Leu Gln Asn Asn Gln Leu Glu Lys Ile
238          75          80          85
241 Tyr Pro Glu Glu Leu Ser Arg Leu Gln Arg Leu Glu Thr Leu Asn Leu
242 90          95          100          105
245 Gln Asn Asn Arg Leu Thr Ser Arg Gly Leu Pro Glu Glu Ala Phe Glu
246          110          115          120
249 His Leu Thr Ser Leu Asn Tyr Leu Tyr Leu Ala Asn Asn Lys Leu Thr
250          125          130          135
253 Leu Ala Pro Arg Phe Leu Pro Asn Ala Leu Ile Ser Val Asp Phe Ala
254          140          145          150
257 Ala Asn Tyr Leu Thr Lys Ile Tyr Gly Leu Thr Phe Gly Gln Lys Pro
258          155          160          165
261 Asn Leu Arg Ser Val Tyr Leu His Asn Asn Lys Leu Ala Asp Ala Gly
262 170          175          180          185
265 Leu Pro Asp His Met Phe Asn Gly Ser Ser Asn Val Glu Ile Leu Ile
266          190          195          200
269 Leu Ser Ser Asn Phe Leu Arg His Val Pro Lys His Leu Pro Pro Ala
270          205          210          215
273 Leu Tyr Lys Leu His Leu Lys Asn Asn Lys Leu Glu Lys Ile Pro Pro
274          220          225          230
277 Gly Ala Phe Ser Glu Leu Ser Asn Leu Arg Glu Leu Tyr Leu Gln Asn
278          235          240          245

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RAW SEQUENCE LISTING

DATE: 01/19/2005

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Input Set : A:\3083us0p.seq.txt

Output Set: N:\CRF4\01192005\J520783.raw

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281 Asn Tyr Leu Thr Asp Glu Gly Leu Asp Asn Glu Thr Phe Trp Lys Leu
282 250                255                260                265
285 Ser Ser Leu Glu Tyr Leu Asp Leu Ser Ser Thr Asn Leu Ser Arg Val
286                270                275                280
289 Pro Ala Gly Leu Pro Arg Ser Leu Val Leu Leu His Leu Glu Lys Asn
290                285                290                295
293 Ala Ile Gln Ser Val Glu Ala Asp Val Leu Thr Pro Ile Arg Asn Leu
294                300                305                310
297 Glu Tyr Leu Leu Leu His Ser Asn Gln Leu Gln Ala Lys Gly Ile His
298                315                320                325
301 Pro Leu Ala Phe Gln Gly Leu Lys Lys Leu His Thr Val His Leu Tyr
302 330                335                340                345
305 Asn Asn Ala Leu Glu Arg Val Pro Ser Gly Leu Pro Arg Arg Val Arg
306                350                355                360
309 Thr Leu Met Ile Leu His Asn Gln Ile Thr Gly Ile Gly Arg Glu Asp
310                365                370                375
313 Phe Ala Thr Thr Tyr Phe Leu Glu Glu Leu Asn Leu Ser Tyr Asn Arg
314                380                385                390
317 Ile Thr Ser Pro Gln Met His Arg Asp Ala Phe Arg Lys Leu Arg Leu
318                395                400                405
321 Leu Arg Ser Leu Asp Leu Ser Gly Asn Arg Leu Gln Thr Leu Pro Pro
322 410                415                420                425
325 Gly Leu Pro Lys Asn Val His Val Leu Lys Val Lys Arg Asn Glu Leu
326                430                435                440
329 Ala Ala Leu Ala Arg Gly Ala Leu Ala Gly Met Ala Gln Leu Arg Glu
330                445                450                455
333 Leu Tyr Leu Thr Gly Asn Arg Leu Arg Ser Arg Ala Leu Gly Pro Arg
334                460                465                470
337 Ala Trp Val Asp Leu Ala Gly Leu Gln Leu Leu Asp Ile Ala Gly Asn
338                475                480                485
341 Gln Leu Thr Glu Val Pro Glu Gly Leu Pro Pro Ser Leu Glu Tyr Leu
342 490                495                500                505
345 Tyr Leu Gln Asn Asn Lys Ile Ser Ala Val Pro Ala Asn Ala Phe Asp
346                510                515                520
349 Ser Thr Pro Asn Leu Lys Gly Ile Phe Leu Arg Phe Asn Lys Leu Ala
350                525                530                535
353 Val Gly Ser Val Val Glu Ser Ala Phe Arg Arg Leu Lys His Leu Gln
354                540                545                550
357 Val Leu Asp Ile Glu Gly Asn Phe Glu Phe Gly Asn Gly Ser Lys Asp
358                555                560                565
361 Lys Asp Glu Glu Glu Glu Glu Glu Glu Glu Glu Asp Glu Glu Glu
362 570                575                580                585
365 Glu Thr Arg
369 <210> SEQ ID NO: 3
370 <211> LENGTH: 480
371 <212> TYPE: DNA
372 <213> ORGANISM: Mus musculus
374 <220> FEATURE:
375 <221> NAME/KEY: CDS

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RAW SEQUENCE LISTING ERROR SUMMARY

DATE: 01/19/2005

PATENT APPLICATION: US/10/520,783

TIME: 12:00:56

Input Set : A:\3083us0p.seq.txt

Output Set: N:\CRF4\01192005\J520783.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 798

Seq#:23; N Pos. 633,680,682

Seq#:25; N Pos. 662

Seq#:27; N Pos. 325,329

Seq#:29; N Pos. 605

Seq#:30; N Pos. 589

VERIFICATION SUMMARY

DATE: 01/19/2005

PATENT APPLICATION: US/10/520,783

TIME: 12:00:56

Input Set : A:\3083us0p.seq.txt

Output Set: N:\CRF4\01192005\J520783.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:37 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:30
L:42 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:35
L:48 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:40
L:113 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:768
L:384 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:377
L:389 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:382
L:389 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:387
L:493 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:486
L:498 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:491
L:498 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:496
L:706 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:699
L:711 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:704
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L:903 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:896
L:908 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:901
L:908 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:906
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L:1526 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:15,Line#:1519
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L:2023 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:21,Line#:2016
L:2028 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:21,Line#:2021
L:2028 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:21,Line#:2026
L:2609 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:600
M:341 Repeated in SeqNo=23
L:2675 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:660
L:2751 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:300
L:2827 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29 after pos.:600
L:2870 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:540
L:3094 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:47